

Art Unit: 1652

## APPENDIX A

AC P35749; O00396; O94944; P78422;

Query Match 98.5%; Score 3564.5; DB 1; Length 1972;  
Best Local Similarity 99.0%; Pred. No. 1.2e-211;  
Matches 692; Conservative 0; Mismatches 0; Indels 7; Gaps 1;

Qy 1 MAQKGQLSDDEKFLFVDKNFINSVPAQADWAAKRLVWVPSEKQGFEEAASKEEKGDEVVV 60  
|||  
Db 1 MAQKGQLSDDEKFLFVDKNFINSVPAQADWAAKRLVWVPSEKQGFEEAASKEEKGDEVVV 60

Qy 61 ELVENGKKVTVGKDDIQMNPFPKFSKVEDMAELTCLNEASVLHNLRLRERYFSGLIYTYSGL 120  
|||  
Db 61 ELVENGKKVTVGKDDIQMNPFPKFSKVEDMAELTCLNEASVLHNLRLRERYFSGLIYTYSGL 120

Qy 121 FCVVVNPYKHLPIYSEKIVDMYKGKKRHEMPPHIYAIADTAYRSMQLQDREDQSILCTGES 180  
|||  
Db 121 FCVVVNPYKHLPIYSEKIVDMYKGKKRHEMPPHIYAIADTAYRSMQLQDREDQSILCTGES 180

Qy 181 GAGKTENTKKVIQYLAVVASSHKGKDTSTITQGPSFAYGELEKQLLQANPILEAFGNAKT 240  
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Db 181 GAGKTENTKKVIQYLAVVASSHKGKDTSTIT-----GELEKQLLQANPILEAFGNAKT 233

Qy 241 VKNDNSSRFGKFIRINFVDTGYIVGANIETYLLEKSRAIRQARDERTFHIFYMIAGAKE 300  
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Db 234 VKNDNSSRFGKFIRINFVDTGYIVGANIETYLLEKSRAIRQARDERTFHIFYMIAGAKE 293

Qy 301 KMRSDDLLEGFNNYTFLSNGFVPIPAAQDDEMFQETVEAMAIMGFSEEEQLSILKVVSSV 360  
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Db 294 KMRSDDLLEGFNNYTFLSNGFVPIPAAQDDEMFQETVEAMAIMGFSEEEQLSILKVVSSV 353

Qy 361 LQLGNIVFKKERNTDQASMPDNTAAQKVCHLMGINVTDFTRSILTPRIKVGRDVVQKAQT 420  
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Db 354 LQLGNIVFKKERNTDQASMPDNTAAQKVCHLMGINVTDFTRSILTPRIKVGRDVVQKAQT 413

Qy 421 KEQADFAVEALAKATYERLFRWILTRVNKALDKTHRQASFLGILDIAQFEIFEVNSFEQ 480  
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Db 414 KEQADFAVEALAKATYERLFRWILTRVNKALDKTHRQASFLGILDIAQFEIFEVNSFEQ 473

Qy 481 LCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGLDLQPCIELIERPNNPPGVLA 540  
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Db 474 LCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGLDLQPCIELIERPNNPPGVLA 533

Qy 541 LLDEECWFPAKTDKSFVEKLCTEQGSHPKFKPKQLKDKTEFSIIHYAGKVDYNASAWLT 600  
|||  
Db 534 LLDEECWFPAKTDKSFVEKLCTEQGSHPKFKPKQLKDKTEFSIIHYAGKVDYNASAWLT 593

Qy 601 KNMDPLNDNVTSLLNASSDKFVADLWKDVDRIVGLDQMAKMTESLPSASKTKKGMFRTV 660  
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Db 594 KNMDPLNDNVTSLLNASSDKFVADLWKDVDRIVGLDQMAKMTESLPSASKTKKGMFRTV 653

Qy 661 GQLYKEQLGKLMTTLRNTTPNFVRCIIPNHEKRSGKLD 699  
|||  
Db 654 GQLYKEQLGKLMTTLRNTTPNFVRCIIPNHEKRSGKLD 692

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**APPENDIX B**

AB020673  
FEATURES

source	1. .6846 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="hk00546s1" /tissue_type="brain" /clone_lib="pBluescriptII SK plus"
gene	1. .6846 /gene="KIAA0866"
CDS	<40. .5994 /gene="KIAA0866" /note="This sequence was replaced that of hk06733 cDNA as a representative cDNA sequence for KIAA0866." /codon_start=1 /product="KIAA0866 protein" /protein_id="BAA74889.2" /db_xref="GI:27529744" /translation="SPQLEIWDQQGTMAQKGLSDDEKFLFVDKNFINSPPVAQADWAA KRLVWVPSEKQGFEEAASIKKEKGDEVVVELVENGKKVTVGKDDIQKMNPPKFSKVEDM AELTCLNEASVLHNLRLRERYFSGLIYTYSGLCFVVVNPYKHLPIYSEKIVDMYKGGKRH EMPHIYAIADTAYRSMQLQDREDQSILCTGESGAGKTENTKKVIQYLAVVASSHKGKK DTSITGELEKQLLQANPILEAFGNAKTVKNDNSSRFGKFIRINFDVTGYIVGANIETY LLEKSRAIRQARDERTFHFYMIAGAKEKMRSDLLLEGFNNTFLSNGFVPIPAQD DEMFQETVEAMAIMGFSEEEQLSILKVVSSVLQLGNIVFKKERNTDQASMPDNTAAQK VCHLMGINVTDFTSRILTIPRIKVGDRVQKAQTKQADFAVEALAKATYERLFRWILT RVNKALDKTHRQASFLGILDIAQFEIFEVNSFEQLCINYNTEKQLQFLNHTMFILEQ EEYQREGIEWNFIDFGDLQPCIELIERPNNPPGVALLDEECWFPKATDKSFVEKLC TEQGSHPKFKPKQLKDKTEFSIIHYAGKVDYNASAWLTKNMDPLNDNVTSLNASSD KFVADLWKDVRIVGLDQMAKMTESLPSASKTKKGMFRTVGQLYKEQLGKLMTTLRN TTPNFVRCIIPNHEKRSGLDAFLVLEQLRCNGVLEGIRICRQGFPPNRIVFQEFQRQY EILAANAIPKGFMDGKQACILMIKALELDPNLYRIGQSKIFFRTGVLAHLEEEEDLKI TDVIMAFQAMCRGYLARKAFKRQQQLTAMKVIQRNCAAYLKLNRNQQWRLFTKVKPL LQVTRQEEEMQAKEDLQKTKERQKKAENELKELEQKHSQLEEKNLQEQQLQAEDEL YAEAEEMRVRLAAKKQEELEELIHEMEARLEEEEDRQQLQAEKKAQMLDLBEEQLE EEEAARQKLQLEKVTAEAKIKKLEDEILVMDQNNKLSKERKLEERISDLTTNLAEE EEKAKNLTCLKNKHESMISELEVRLLKKEEKSQRQLEKLRKLEGDASDFHEQIADLQA QIAELKMLAKKEEELQAALARLDDEIAQKNNAKKIRELEGHIIDLQEDLDSERAAR NKAQKQKRDLEGELEALKTELEDTLSTATQQLRAKREQEVTVLKKALDEETRSHEA QVQEMRQKHAQAVEELTEQLEQFKRAKANLDKNKQTLKENADLAGELRVLGQAKQEV EHKKKKLEAQVQELQSKCSDGERARAEELNDKVHKLQNEVESVTGMLNEAEGKAIKLAK DVASLSSQLQDTQELLQEBTRQKLVSTKLRQLEEEERNSLQDQLDEEMEAKQNLERHI STLNIQLSDSKKKLQDFASTVEALEEGKKRFQKEIENLTQQYEEKAAAYDKLEKTKNR LQQELDDLVDLDNRQLVSNLEKKQRKFDQLLAEKNISSEYADERDRAEAEAREKE TKALSLARALEEAEKEELERTNKMKAEMEDLVSSKDDVGKNVHELEKSKRALETQ MEEMKTQLEEELEDELQATEDAKLRLEVNMQALKGQFERDLQARDEQNEEKRRQLQRQL HEYETELEDERKQALAAAANKKLEGLDKDELQADSAIKGEEAIKQLRKLQAQMKD FQRELEDARASRDEIFATAKENEKKAKSLEADLMQLQEDLAAAERARKQADLEKEELA EELASSLSGRNALQDEKRRLEARIAQLEEELEEEQGNMEAMSDVRKATQQAQELSNE LATERSTAQKNESARQLEKQKELRSKLHEMEGAVKSKFKSTIAALEAKIAQLEEQV EQEAREKQAATKSLKQKDKKLKEILLQVEDERKMAEQYKEQAEKGNARVKQLKRQLEE AEESQRINANRRKLQRELDEATESNEAMGREVNALKSKLRRGNETSFPVPSRRSGGRR VIENADGSEETDTRDADFNKASE"

**ORIGIN****Alignment Scores:**

Pred. No.:	3.95e-263	Length:	6846
Score:	3564.50	Matches:	692
Percent Similarity:	99.00%	Conservative:	0
Best Local Similarity:	99.00%	Mismatches:	0
Query Match:	98.55%	Indels:	7
DB:	9	Gaps:	1

US-09-927-597-6 (1-699) x AB020673 (1-6846)

Qy	1	MetAlaGlnLysGlyGlnLeuSerAspAspGluLysPheLeuValAspLysAsnPhe	20
Db	76	ATGGCGCAGAAGGGCCAACTCAGTGACGATGAGAAGTTCCTCTTTGTGGACAAAACTTC	135
Qy	21	IleAsnSerProValAlaGlnAlaAspTrpAlaAlaLysArgLeuValTrpValProSer	40
Db	136	ATCAACAGCCCACTGGCCCAAGGCTGACTGGGCGCCCAAGAGACTCGTCTGGGTCCCTCG	195
Qy	41	GluLysGlnGlyPheGluAlaAlaSerIleLysGluGluLysGlyAspGluValValVal	60
Db	196	GAGAAGCAGGGCTTCGAGGCAGCCAGCATTAAAGAGGAGAAGGGGATGAGGTGGTTGTG	255
Qy	61	GluLeuValGluAsnGlyLysLysValThrValGlyLysAspAspIleGlnLysMetAsn	80
Db	256	GAGCTGGTGAGAAATGGCAAGAAGGTACGGTTGGGAAAGATGACATCCAGAAGATGAAC	315
Qy	81	ProProLysPheSerLysValGluAspMetAlaGluLeuThrCysLeuAsnGluAlaSer	100
Db	316	CCACCCAAGTTCTCCAAGGTGGAGGACATGGCGGAGCTGACGTGCCTCAACGAAGCCTCC	375
Qy	101	ValLeuHisAsnLeuArgGluArgTyrPheSerGlyLeuIleTyrThrTyrSerGlyLeu	120
Db	376	GTGTACACAACCTTGAGGGAGCGGTACTTCTCAGGGCTAATATATACGTACTCTGGCCTC	435
Qy	121	PheCysValValValAsnProTyrLysHisLeuProIleTyrSerGluLysIleValAsp	140
Db	436	TTCTGCGTGGTGGTCAACCCCTATAAACACCTGCCCATCTACTCGGAGAAGATCGTCGAC	495
Qy	141	MetTyrLysGlyLysLysArgHisGluMetProProHisIleTyrAlaIleAlaAspThr	160
Db	496	ATGTACAAGGGCAAGAAGAGGCACGAGATGCCGCCTCACATCTACGCCATCGCAGACACG	555
Qy	161	AlaTyrArgSerMetLeuGlnAspArgGluAspGlnSerIleLeuCysThrGlyGluSer	180
Db	556	GCCTACCGGAGCATGCTTCAAGATCGGGAGGACCAGTCCATTCTATGCACAGGCGAGTCT	615
Qy	181	GlyAlaGlyLysThrGluAsnThrLysLysValIleGlnTyrLeuAlaValValAlaSer	200
Db	616	GGAGCCGGGAAACCGAAAACACCAAGAAGGTCATTACAGTACCTGGCCGTGGTGGCCTCC	675
Qy	201	SerHisLysGlyLysLysAspThrSerIleThrGlnGlyProSerPheAlaTyrGlyGlu	220
Db	676	TCCACAAGGGCAAGAAAGACACAAGTATCAGG-----GGAGAG	714
Qy	221	LeuGluLysGlnLeuLeuGlnAlaAsnProIleLeuGluAlaPheGlyAsnAlaLysThr	240
Db	715	CTGGAAAAGCAGCTTCTACAAGCAAACCCGATTCTGGAGGCTTTCGGCAACGCCAAAACA	774
Qy	241	ValLysAsnAspAsnSerSerArgPheGlyLysPheIleArgIleAsnPheAspValThr	260
Db	775	GTGAAGAACGACAACCTCCTCAGGATTCGGCAAATTCATCCGCATCAACTTCGACGTCACG	834
Qy	261	GlyTyrIleValGlyAlaAsnIleGluThrTyrLeuLeuGluLysSerArgAlaIleArg	280
Db	835	GGTTACATCGTGGGAGCCAACATTGAGACCTATCTGCTAGAAAAATCACGGGCAATTGCG	894
Qy	281	GlnAlaArgAspGluArgThrPheHisIlePheTyrTyrMetIleAlaGlyAlaLysGlu	300
Db	895	CAAGCCAGAGACGAGAGGACATTCACATCTTTTACTACATGATTGCTGGAGCCAAGGAG	954
Qy	301	LysMetArgSerAspLeuLeuLeuGluGlyPheAsnAsnTyrThrPheLeuSerAsnGly	320
Db	955	AAGATGAGAAGTGACTTGCTTTTGGAGGGCTTCAACAACTACACCTTCTCTCCAATGGC	1014
Qy	321	PheValProIleProAlaAlaGlnAspAspGluMetPheGlnGluThrValGluAlaMet	340
Db	1015	TTTGTGCCCATCCAGCAGCCAGGATGATGAGATGTTCCAGGAAACCGTGGAGGCCATG	1074
Qy	341	AlaIleMetGlyPheSerGluGluGluGlnLeuSerIleLeuLysValValSerSerVal	360

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      |||
Db      1075 GCAATCATGGGTTTCAGCGAGGAGGAGCAGCTATCCATATTGAAGGTGGTATCATCGGTC 1134
Qy      361 LeuGlnLeuGlyAsnIleValPheLysLysGluArgAsnThrAspGlnAlaSerMetPro 380
      |||
Db      1135 CTGCAGCTTGGAATATCGTCTTCAAGAAGGAAAGAAACACAGACCAGGCGTCCATGCCA 1194
Qy      381 AspAsnThrAlaAlaGlnLysValCysHisLeuMetGlyIleAsnValThrAspPheThr 400
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Db      1195 GATAACACAGCTGCTCAGAAAGTTTGCCACCTCATGGGAATTAATGTGACAGATTTCACC 1254
Qy      401 ArgSerIleLeuThrProArgIleLysValGlyArgAspValValGlnLysAlaGlnThr 420
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Db      1255 AGATCCATCCTCACTCCTCGTATCAAGGTGGGCGAGATGTGGTACAGAAAGCTCAGACA 1314
Qy      421 LysGluGlnAlaAspPheAlaValGluAlaLeuAlaLysAlaThrTyrGluArgLeuPhe 440
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Db      1315 AAAGAACAGGCTGACTTTGCTGTAGAGGCTTTGGCCAAGGCAACATATGAGCGCCTTTTC 1374
Qy      441 ArgTrpIleLeuThrArgValAsnLysAlaLeuAspLysThrHisArgGlnGlyAlaSer 460
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Db      1375 CGCTGGATACTACCCGCGTGAACAAAGCCCTGGACAAGACCCATCGGCAAGGGGCTTCC 1434
Qy      461 PheLeuGlyIleLeuAspIleAlaGlyPheGluIlePheGluValAsnSerPheGluGln 480
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Qy      481 LeuCysIleAsnTyrThrAsnGluLysLeuGlnGlnLeuPheAsnHisThrMetPheIle 500
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Db      1495 CTGTGCATCAACTACCAACGAGAAGCTGCAGCAGCTCTTCAACCACCATGTTTCATC 1554
Qy      501 LeuGluGlnGluGluTyrGlnArgGluGlyIleGluTrpAsnPheIleAspPheGlyLeu 520
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Qy      521 AspLeuGlnProCysIleGluLeuIleGluArgProAsnAsnProProGlyValLeuAla 540
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Qy      541 LeuLeuAspGluGluCysTrpPheProLysAlaThrAspLysSerPheValGluLysLeu 560
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Db      1675 CTGCTGGACGAGGAATGCTGTTCCCAAAGCCACGACAAGTCTTTCGTGGAGAAGCTG 1734
Qy      561 CysThrGluGlnGlySerHisProLysPheGlnLysProLysGlnLeuLysAspLysThr 580
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Db      1735 TGCACGGAGCAGGGCAGCCACCCCAAGTTCAGAAGCCCAAGCAGCTCAAGGACAAGACT 1794
Qy      581 GluPheSerIleIleHisTyrAlaGlyLysValAspTyrAsnAlaSerAlaTrpLeuThr 600
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Db      1795 GAGTTCTCCATCATCCATTATGCTGGGAAGGTGGACTATAATGCGAGTGCCTGGCTGACC 1854
Qy      601 LysAsnMetAspProLeuAsnAspAsnValThrSerLeuLeuAsnAlaSerSerAspLys 620
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Db      1855 AAGAATATGGACCCGCTGAATGACAACGTGACTTCCCTGCTCAATGCCTCCTCCGACAAG 1914
Qy      621 PheValAlaAspLeuTrpLysAspValAspArgIleValGlyLeuAspGlnMetAlaLys 640
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Db      1915 TTTGTGGCCGACCTGTGGAAGGACGTGGACCGCATCGTGGGCTTGACACAGATGGCCAAG 1974
Qy      641 MetThrGluSerSerLeuProSerAlaSerLysThrLysLysGlyMetPheArgThrVal 660
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Db      1975 ATGACGGAGAGCTCGCTGCCAGCGCCTCCAAGACCAAGAAGGGCATGTTCCGCACAGTG 2034
Qy      661 GlyGlnLeuTyrLysGluGlnLeuGlyLysLeuMetThrThrLeuArgAsnThrThrPro 680
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Db      2035 GGGCAGCTGTACAAGGAGCAGCTGGGCAAGCTGATGACCACGCTACGCAACACCACGCCC 2094
Qy      681 AsnPheValArgCysIleIleProAsnHisGluLysArgSerGlyLysLeuAspAla 699
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Db 2095 AACTTCGTGCGCTGCATCATCCCCAACCACGAGAAGAGGTCCGGCAAGCTGGATGCG 2151